

## SEQUENCE LISTING

&lt;110&gt; Reinhard, Christoph

&lt;120&gt; HUMAN CYCLIN-DEPENDANT KINASE (hPNQALRE)

&lt;130&gt; 200130.459

&lt;140&gt; US 09/464,065

&lt;141&gt; 1999-12-15

&lt;160&gt; 17

&lt;170&gt; FastSEQ for Windows Version 4.0

&lt;210&gt; 1

&lt;211&gt; 1002

&lt;212&gt; DNA

&lt;213&gt; Homo sapien

&lt;400&gt; 1

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gagatggagg acaatcagta tgtggtacaa ctgaaggctg tgttcccaca cgggtggaggc      240
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&lt;210&gt; 2

&lt;211&gt; 325

&lt;212&gt; PRT

&lt;213&gt; Homo sapien

&lt;400&gt; 2

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Met Asp Gln Tyr Cys Ile Leu Gly Arg Ile Gly Glu Gly Ala His Gly
  1             5             10             15
Ile Val Phe Lys Ala Lys His Val Glu Thr Gly Glu Ile Val Ala Leu
      20             25             30
Lys Lys Val Ala Leu Arg Arg Leu Glu Asp Gly Phe Pro Asn Gln Ala
      35             40             45
Leu Arg Glu Ile Lys Ala Leu Gln Glu Met Glu Asp Asn Gln Tyr Val

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50		55		60
Val Gln Leu Lys Ala	Val Phe Pro His Gly Gly Gly Phe Val Leu Ala			
65	70	75	80	
Phe Glu Phe Met Leu Ser Asp Leu Ala Glu Val Val Arg His Ala Gln				
	85	90	95	
Arg Pro Leu Ala Gln Ala Gln Val Lys Ser Tyr Leu Gln Met Leu Leu				
	100	105	110	
Lys Gly Val Ala Phe Cys His Ala Asn Asn Ile Val His Arg Asp Leu				
	115	120	125	
Lys Pro Ala Asn Leu Leu Ile Ser Ala Ser Gly Gln Leu Lys Ile Ala				
	130	135	140	
Asp Phe Gly Leu Ala Arg Val Phe Ser Pro Asp Gly Ser Arg Leu Tyr				
145	150	155	160	
Thr His Gln Val Ala Thr Arg Ser Val Gly Cys Ile Met Gly Glu Leu				
	165	170	175	
Leu Asn Gly Ser Pro Leu Phe Pro Gly Lys Asn Asp Ile Glu Gln Leu				
	180	185	190	
Cys Tyr Val Leu Arg Ile Leu Gly Thr Pro Asn Pro Gln Val Trp Pro				
	195	200	205	
Glu Leu Thr Glu Leu Pro Asp Tyr Asn Lys Ile Ser Leu Lys Glu Gln				
	210	215	220	
Val Pro Met Pro Leu Glu Val Leu Pro Asp Val Ser Pro Gln Ala				
225	230	235	240	
Leu Asp Leu Leu Gly Gln Phe Leu Leu Tyr Pro Pro His Gln Arg Ile				
	245	250	255	
Ala Ala Ser Lys Ala Leu Leu His Gln Tyr Phe Phe Thr Ala Pro Leu				
	260	265	270	
Pro Ala His Pro Ser Glu Leu Pro Ile Pro Gln Arg Leu Gly Gly Pro				
	275	280	285	
Ala Pro Lys Ala His Pro Gly Pro Pro His Ile His Asp Phe His Val				
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Asp Arg Pro Leu Glu Glu Ser Leu Leu Asn Pro Glu Leu Ile Arg Pro				
305	310	315	320	
Phe Ile Leu Glu Arg				
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<210> 3  
 <211> 1053  
 <212> DNA  
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aatcagtatg tggtaacaact gaaggctgtg ttcccacacg gtggaggctt tgtgctggcc	240
tttgagttca tgctgtcgga tctggccgag gtggtgcgcc atgcccagag gccgctagcc	300
caggcacagg tcaagagcta cctgcagatg ctgctcaagg gtgtcgccct ctgccatgcc	360
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<210> 4

<211> 346

<212> PRT

<213> Homo sapien

<400> 4

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Ile Val Phe Lys Ala Lys His Val Glu Thr Gly Glu Ile Val Ala Leu
          20          25          30
Lys Lys Val Ala Leu Arg Arg Leu Glu Asp Gly Phe Pro Asn Gln Ala
          35          40          45
Leu Arg Glu Ile Lys Ala Leu Gln Glu Met Glu Asp Asn Gln Tyr Val
          50          55          60
Val Gln Leu Lys Ala Val Phe Pro His Gly Gly Gly Phe Val Leu Ala
65          70          75          80
Phe Glu Phe Met Leu Ser Asp Leu Ala Glu Val Val Arg His Ala Gln
          85          90          95
Arg Pro Leu Ala Gln Ala Gln Val Lys Ser Tyr Leu Gln Met Leu Leu
          100          105          110
Lys Gly Val Ala Phe Cys His Ala Asn Asn Ile Val His Arg Asp Leu
          115          120          125
Lys Pro Ala Asn Leu Leu Ile Ser Ala Ser Gly Gln Leu Lys Ile Ala
          130          135          140
Asp Phe Gly Leu Ala Arg Val Phe Ser Pro Asp Gly Ser Arg Leu Tyr
          145          150          155          160
Thr His Gln Val Ala Thr Arg Trp Tyr Arg Ala Pro Glu Leu Leu Tyr
          165          170          175
Gly Ala Arg Gln Tyr Asp Gln Gly Val Asp Leu Trp Ser Val Gly Cys
          180          185          190
Ile Met Gly Glu Leu Leu Asn Gly Ser Pro Leu Phe Pro Gly Lys Asn
          195          200          205
Asp Ile Glu Gln Leu Cys Tyr Val Leu Arg Ile Leu Gly Thr Pro Asn
          210          215          220
Pro Gln Val Trp Pro Glu Leu Thr Glu Leu Pro Asp Tyr Asn Lys Ile
          225          230          235          240
Ser Phe Lys Glu Gln Val Pro Met Pro Leu Glu Glu Val Leu Pro Asp
          245          250          255
Val Ser Pro Gln Ala Leu Asp Leu Leu Gly Gln Phe Leu Leu Tyr Pro
          260          265          270
Pro His Gln Arg Ile Ala Ala Ser Lys Ala Leu Leu His Gln Tyr Phe
          275          280          285
Phe Thr Ala Pro Leu Pro Ala His Pro Ser Glu Leu Pro Ile Pro Gln
          290          295          300
Arg Leu Gly Gly Pro Ala Pro Lys Ala His Pro Gly Pro Pro His Ile
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<210> 6
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          20          25          30
Leu Pro Ser Ile Leu Gln Thr Gly Glu Ile Val Ala Leu Lys Lys Val
          35          40          45
Ala Leu Arg Arg Leu Glu Asp Gly Phe Pro Asn Gln Ala Leu Arg Glu
          50          55          60
Ile Lys Ala Leu Gln Glu Met Glu Asp Asn Gln Tyr Val Val Gln Leu
65          70          75          80
Lys Ala Val Phe Pro His Gly Gly Gly Phe Val Leu Ala Phe Glu Phe
          85          90          95
Met Leu Ser Asp Leu Ala Glu Val Val Arg His Ala Gln Arg Pro Leu
          100          105          110
Ala Gln Ala Gln Val Lys Ser Tyr Leu Gln Met Leu Leu Lys Gly Val
          115          120          125
Ala Phe Cys His Ala Asn Asn Ile Val His Arg Asp Leu Lys Pro Ala
          130          135          140

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Asn Leu Leu Ile Ser Ala Ser Gly Gln Leu Lys Ile Ala Asp Phe Gly  
 145 150 155 160  
 Leu Ala Arg Val Phe Ser Pro Asp Gly Ser Arg Leu Tyr Thr His Gln  
 165 170 175  
 Val Ala Thr Arg Trp Tyr Arg Ala Pro Glu Leu Leu Tyr Gly Ala Arg  
 180 185 190  
 Gln Tyr Asp Gln Gly Val Asp Leu Trp Ser Val Gly Cys Ile Met Gly  
 195 200 205  
 Glu Leu Leu Asn Gly Ser Pro Leu Phe Pro Gly Lys Asn Asp Ile Glu  
 210 215 220  
 Gln Leu Cys Tyr Val Leu Arg Ile Leu Gly Thr Pro Asn Pro Gln Val  
 225 230 235 240  
 Trp Pro Glu Leu Thr Glu Leu Pro Asp Tyr Asn Lys Ile Ser Phe Lys  
 245 250 255  
 Glu Gln Val Pro Met Pro Leu Glu Glu Val Leu Pro Asp Val Ser Pro  
 260 265 270  
 Gln Ala Leu Asp Leu Leu Gly Gln Phe Leu Leu Tyr Pro Pro His Gln  
 275 280 285  
 Arg Ile Ala Ala Ser Lys Ala Leu Leu His Gln Tyr Phe Phe Thr Ala  
 290 295 300  
 Pro Leu Pro Ala His Pro Ser Glu Leu Pro Val Pro Gln Arg Leu Gly  
 305 310 315 320  
 Gly Pro Ala Pro Lys Ala His Pro Gly Pro Pro His Ile His Asp Phe  
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 Arg Pro Phe Ile Leu Glu Gly  
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<210> 7

<211> 1038

<212> DNA

<213> Homo sapien

<400> 7

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gccctgcggg	agattaaggc	tctgcaggag	atggaggaca	atcagtatgt	ggtacaactg	240
aaggctgtgt	tcccacacgg	tggaggcttt	gtgctggcct	ttgagttcat	gctgtcggat	300
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ctgcagatgc	tgtcaagg	tgtgccttc	tgccatgcca	acaacattgt	acatcgggac	420
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 35 40 45  
 Ala Leu Arg Arg Leu Glu Asp Gly Phe Pro Asn Gln Ala Leu Arg Glu  
 50 55 60  
 Ile Lys Ala Leu Gln Glu Met Glu Asp Asn Gln Tyr Val Val Gln Leu  
 65 70 75 80  
 Lys Ala Val Phe Pro His Gly Gly Gly Phe Val Leu Ala Phe Glu Phe  
 85 90 95  
 Met Leu Ser Asp Leu Ala Glu Val Val Arg His Ala Gln Arg Pro Leu  
 100 105 110  
 Ala Gln Ala Gln Val Lys Ser Tyr Leu Gln Met Leu Leu Lys Gly Val  
 115 120 125  
 Ala Phe Cys His Ala Asn Asn Ile Val His Arg Asp Leu Lys Pro Ala  
 130 135 140  
 Asn Leu Leu Ile Ser Ala Ser Gly Gln Leu Lys Ile Ala Asp Phe Gly  
 145 150 155 160  
 Leu Ala Arg Val Phe Ser Pro Asp Gly Ser Arg Leu Tyr Thr His Gln  
 165 170 175  
 Val Ala Thr Arg Trp Tyr Arg Ala Pro Glu Leu Leu Tyr Gly Ala Arg  
 180 185 190  
 Gln Tyr Asp Gln Gly Val Asp Leu Trp Ser Val Gly Cys Ile Met Gly  
 195 200 205  
 Glu Leu Leu Asn Gly Ser Pro Leu Phe Pro Gly Lys Asn Asp Ile Glu  
 210 215 220  
 Gln Leu Cys Tyr Val Leu Arg Ile Leu Gly Thr Pro Asn Pro Gln Val  
 225 230 235 240  
 Trp Pro Glu Gln Val Pro Met Pro Leu Glu Glu Val Leu Pro Asp Val  
 245 250 255  
 Ser Pro Gln Ala Leu Asp Leu Leu Gly Gln Phe Leu Leu Tyr Pro Pro  
 260 265 270  
 His Gln Arg Ile Ala Ala Ser Lys Ala Leu Leu His Gln Tyr Phe Phe  
 275 280 285  
 Thr Ala Pro Leu Pro Ala His Pro Ser Glu Leu Pro Ile Pro Gln Arg  
 290 295 300  
 Leu Gly Gly Pro Ala Pro Lys Ala His Pro Gly Pro Pro His Ile His  
 305 310 315 320  
 Asp Phe His Val Asp Arg Pro Leu Glu Glu Ser Leu Leu Asn Pro Glu  
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 Leu Ile Arg Pro Phe Ile Leu Glu Gly  
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<210> 9  
 <211> 7  
 <212> PRT

<213> Unknown

<220>

<223> Sequence which characterizes the cyclin binding domain of cyclin-dependant kinases.

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Pro Asn Gln Ala Leu Arg Glu  
1 5

<210> 10

<211> 7

<212> PRT

<213> Unknown

<220>

<223> Sequence which characterizes the cyclin binding domain of cyclin-dependant kinases.

<400> 10

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<210> 11

<211> 7

<212> PRT

<213> Unknown

<220>

<223> Sequence which characterizes the cyclin binding domain of cyclin-dependant kinases.

<400> 11

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<210> 12

<211> 7

<212> PRT

<213> Unknown

<220>

<223> Sequence which characterizes the cyclin binding domain of cyclin-dependant kinases.

<400> 12

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<210> 13

<211> 7

<212> PRT

<213> Unknown

<220>

<223> Sequence which characterizes the cyclin binding domain of cyclin-dependant kinases.

<400> 13

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<210> 14

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<213> Unknown

<220>

<223> Sequence which characterizes the cyclin binding domain of cyclin-dependant kinases.

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<210> 15

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<212> PRT

<213> Unknown

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<223> Sequence which characterizes the cyclin binding domain of cyclin-dependant kinases.

<400> 15

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<210> 16

<211> 7

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<213> Unknown

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<223> Sequence which characterizes the cyclin binding domain of cyclin-dependant kinases.

<400> 16

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<210> 17

<211> 21

<212> PRT

<213> Homo sapien

<400> 17

His Asp Phe His Val Asp Arg Pro Leu Glu Glu Ser Leu Ile Asn Pro



9

1 5  
Glu Leu Ile Arg Pro  
20

10

15